



## SEQUENCE LISTING

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<120> INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT

<130> 2879-US

<140> US 09/835,147

<141> 2001-04-13

<150> US 60/104,585

<151> 1998-10-16

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<150> PCT/US99/22955

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<160> 37

<170> PatentIn version 3.1

<210> 1

<211> 1599

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)..(1596)

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Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser

1

5

10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156

Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile

15

20

25

30

gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204

Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn

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gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252

Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu

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tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300  
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
 65 70 75

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348  
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe  
 80 85 90

gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396  
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu  
 95 100 105 110

aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt 444  
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val  
 115 120 125

tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa 492  
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu  
 130 135 140

gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac 540  
 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn  
 145 150 155

tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa 588  
 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu  
 160 165 170

ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt 636  
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser  
 175 180 185 190

cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag 684  
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln  
 195 200 205

gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act 732  
 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr  
 210 215 220

ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa 780  
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln  
 225 230 235

ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg 828  
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu  
 240 245 250

tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att 876  
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile  
 255 260 265 270

cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga 924  
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly  
 275 280 285

tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc 972  
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr  
 290 295 300

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt 1020  
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly  
 305 310 315

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac 1068  
 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn  
 320 325 330

acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 1116  
 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu  
 335 340 345 350

cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1164  
 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val  
 355 360 365

atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1212  
 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val  
 370 375 380

act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1260  
 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys  
 385 390 395

aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1308  
 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe  
 400 405 410

tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1356  
 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr  
 415 420 425 430

gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1404  
 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser  
 435 440 445

gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1452  
 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile  
 450 455 460

cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc 1500  
 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val  
 465 470 475

ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata 1548  
 Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile  
 480 485 490

ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta 1596  
 Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val  
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tag 1599

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 <211> 510  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn  
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Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu  
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Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu  
465 470 475 480

Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu  
 485 490 495

Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val  
 500 505 510

<210> 3  
 <211> 476  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct of human CD39

<400> 3

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys  
 1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly  
 20 25 30

Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
 35 40 45

*62* Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
 85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
 100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
 115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
 130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
 145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
 165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
 420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
 435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
 450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470 475

<210> 4

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion construct of human CD39

<220>

<221> MISC\_FEATURE

<222> (39)..(39)

<223> Any amino acid, preferably Cys or Ser

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Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly  
 20 25 30

Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu  
 35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
 85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
 100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
 115 120 125



Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
465 470 475

<210> 5  
<211> 1365  
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<220>  
<221> CDS  
<222> (1)..(1362)  
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cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg gat 96  
Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp  
20 25 30  
gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca gaa 144  
Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu  
35 40 45  
aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg gtt 192  
Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val  
50 55 60

aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata ggc 240  
 Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly  
 65 70 75 80

att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca agg 288  
 Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg  
 85 90 95

tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg 336  
 Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met  
 100 105 110

cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat 384  
 Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp  
 115 120 125

gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc 432  
 Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala  
 130 135 140

agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc 480  
 Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile  
 145 150 155 160

aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata 528  
 Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile  
 165 170 175

gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt 576  
 Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu  
 180 185 190

ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act atc 624  
 Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile  
 195 200 205

gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac tac 672  
 Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr  
 210 215 220

aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca ctc 720  
 Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu  
 225 230 235 240

tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att ctc 768  
 Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu  
 245 250 255

agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta agt 816  
 Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser  
 260 265 270

gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt cca 864  
 Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro  
 275 280 285

ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc cat 912  
 Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His  
 290 295 300

caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc cag 960  
 Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln  
 305 310 315 320  
  
 tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt ggg 1008  
 Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly  
 325 330 335  
  
 gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca tca 1056  
 Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser  
 340 345 350  
  
 gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc tgt 1104  
 Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys  
 355 360 365  
  
 gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag gag 1152  
 Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu  
 370 375 380  
  
 aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc ctc 1200  
 Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu  
 385 390 395 400  
  
 ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc cat 1248  
 Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His  
 405 410 415  
  
 ttc att ggc aag atc cag ggc agc gac gcc gcc tgg act ttg ggc tac 1296  
 Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr  
 420 425 430  
  
 atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc aca 1344  
 Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr  
 435 440 445  
  
 cct ctc tcc cac tcc acc taa 1365  
 Pro Leu Ser His Ser Thr  
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 <211> 454  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct of human CD39

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Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp  
 20 25 30

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu  
 35 40 45

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val  
50 55 60

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly  
65 70 75 80

Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg  
85 90 95

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met  
100 105 110

Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp  
115 120 125

Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala  
130 135 140

Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile  
145 150 155 160

Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile  
165 170 175

Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu  
180 185 190

Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile  
195 200 205

Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr  
210 215 220

Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu  
225 230 235 240

Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu  
245 250 255

Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser  
260 265 270

Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro  
275 280 285

Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His  
290 295 300

Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln  
305 310 315 320

Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly  
325 330 335

Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser  
340 345 350

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys  
355 360 365

Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu  
370 375 380

Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu  
385 390 395 400

Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His  
405 410 415

Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr  
420 425 430

Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr  
435 440 445

Pro Leu Ser His Ser Thr  
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<210> 7  
<211> 1437  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion construct of human CD39

<220>  
<221> CDS  
<222> (1)..(1434)  
<223>

<400> 7

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 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96  
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Thr Lys  
 20 25 30

aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac 144  
 Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn  
 35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 192  
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
 50 55 60

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 240  
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
 65 70 75 80

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 288  
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe  
 85 90 95

gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 336  
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu  
 100 105 110

aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt 384  
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val  
 115 120 125

tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa 432  
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu  
 130 135 140

gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac 480  
 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn  
 145 150 155 160

tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa 528  
 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu  
 165 170 175

ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt 576  
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser  
 180 185 190

cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag 624  
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln  
 195 200 205

gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act 672  
 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr  
 210 215 220

ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa 720  
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln  
 225 230 235 240

ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg 768  
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu  
 245 250 255

tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att 816  
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile  
 260 265 270

cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga 864  
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly  
 275 280 285

tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc 912  
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr  
 290 295 300

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt 960  
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly  
 305 310 315 320

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac 1008  
 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn  
 325 330 335

acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 1056  
 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu  
 340 345 350

cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1104  
 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val  
 355 360 365

atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1152  
 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val  
 370 375 380

act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1200  
 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys  
 385 390 395 400

aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1248  
 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe  
 405 410 415

tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1296  
 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr  
 420 425 430

gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1344  
 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser  
 435 440 445

gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1392  
 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile  
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 465 470 475



<210> 8  
 <211> 478  
 <212> PRT  
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<220>  
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<400> 8

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Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn  
 35 40 45

Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
 50 55 60

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
 65 70 75 80

His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe  
 85 90 95

Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu  
 100 105 110

Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val  
 115 120 125

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu  
 130 135 140

Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn  
 145 150 155 160

Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu  
 165 170 175

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser  
 180 185 190

Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln  
 195 200 205

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr  
 210 215 220

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln  
 225 230 235 240

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu  
 245 250 255

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile  
 260 265 270

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly  
 275 280 285

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr  
 290 295 300

Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly  
 305 310 315 320

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn  
 325 330 335

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu  
 340 345 350

Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val  
 355 360 365

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val  
 370 375 380

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys  
 385 390 395 400

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe  
 405 410 415

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr  
 420 425 430

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser  
 435 440 445

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile  
 450 455 460

Pro Ala Glu Gln Pro<sup>o</sup>Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470 475

<210> 9  
 <211> 24  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser  
 20

<210> 10  
 <211> 8  
 <212> PRT  
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<220>  
 <223> Synthetic peptide

<400> 10

Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 11  
 <211> 43  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct of human CD39

<400> 11

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys  
 35 40

<210> 12  
 <211> 29  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct of human CD39

<400> 12

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys  
 20 25

<210> 13  
 <211> 31  
 <212> PRT  
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<220>  
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<400> 13

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys  
 20 25 30

<210> 14  
 <211> 87  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 14  
 ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60  
 tgtccacacc tctctcccac gagcccc 87

<210> 15  
 <211> 87  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 15  
 gatcggggct cgtgggagag aggtgtggac aatgggttgct cagctgggat catgttggtc 60

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<210> 16
<211> 740
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (42) .. (737)
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					1				5							
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	gcc	gag	ggc	104
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	Gly	
				10					15					20		
gcg	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	152
Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			25					30					35			
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	200
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
		40					45					50				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	248
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
	55					60					65					
cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	296
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
	70				75					80					85	
cgg	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	344
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				90					95					100		
aag	gac	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atg	392
Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Met	
			105					110					115			
cag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	440
Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		120				125						130				
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	488
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
	135					140					145					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agg	cac	atc	gcc	gtg	gag	536
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg	His	Ile	Ala	Val	Glu	
	150				155				160						165	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	584
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	

170										175					180					
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	632				
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val					
			185						190					195						
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	680				
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met					
		200					205					210								
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	728				
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser					
	215						220				225									
ccg	ggt	aaa	tga													740				
Pro	Gly	Lys																		
230																				

<210> 17  
 <211> 232  
 <212> PRT  
 <213> Homo sapiens

<400> 17

Glu	Pro	Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
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Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			20					25						30	

Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35					40					45			

Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
	50					55					60				

Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65					70					75					80

Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
				85					90					95	

Asp	Trp	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
			100					105					110		

Leu	Pro	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		115					120						125		

Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
	130						135				140				

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg  
145 150 155 160

His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<210> 18  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide

<400> 18  
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18

<210> 19  
<211> 36  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide

<400> 19  
aaaaaactag tcagaacaaa gctttgccag aaaacg

36

<210> 20  
<211> 24  
<212> PRT  
<213> Mus sp.

<400> 20

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile  
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser

20

<210> 21  
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 <212> DNA  
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<400> 22  
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<210> 23  
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 <212> DNA  
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tgtccacacc tctctcccac tccacctaa 89

<210> 24  
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tcaggttcag catgtagccc aaagtccag 89

<210> 25  
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 <212> DNA  
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&lt;220&gt;

&lt;223&gt; Fusion construct of human CD39

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1461)

&lt;223&gt;

&lt;400&gt; 25

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agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag	96
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys	
20 25 30	

aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa	144
Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Lys	
35 40 45	

acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg	192
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu	
50 55 60	

gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca	240
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala	
65 70 75 80	

gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg	288
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg	
85 90 95	

gtt aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata	336
Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile	
100 105 110	

ggc att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca	384
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro	
115 120 125	

agg tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc	432
Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly	
130 135 140	

atg cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg	480
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu	
145 150 155 160	

gat gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt	528
Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly	
165 170 175	

gcc agg atc att act ggc caa gag gaa ggt gcc tat gcc tgg att act	576
Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr	
180 185 190	

atc aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc	624
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser	
195 200 205	

ata gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac 672  
 Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp  
 210 215 220

ctt ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act 720  
 Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr  
 225 230 235 240

atc gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac 768  
 Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp  
 245 250 255

tac aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca 816  
 Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala  
 260 265 270

ctc tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att 864  
 Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile  
 275 280 285

ctc agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta 912  
 Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val  
 290 295 300

agt gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt 960  
 Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu  
 305 310 315 320

cca ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc 1008  
 Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys  
 325 330 335

cat caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc 1056  
 His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser  
 340 345 350

cag tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt 1104  
 Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe  
 355 360 365

ggg gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca 1152  
 Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr  
 370 375 380

tca gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc 1200  
 Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe  
 385 390 395 400

tgt gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag 1248  
 Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys  
 405 410 415

gag aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc 1296  
 Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser  
 420 425 430

ctc ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc 1344  
 Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile  
 435 440 445

cat ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc 1392

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly  
 450 455 460

tac atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc 1440  
 Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser  
 465 470 475 480

aca cct ctc tcc cac tcc acc taa 1464  
 Thr Pro Leu Ser His Ser Thr  
 485

<210> 26  
 <211> 487  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion construct of human CD39

<400> 26

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys  
 35 40 45

Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu  
 50 55 60

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala  
 65 70 75 80

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg  
 85 90 95

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile  
 100 105 110

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro  
 115 120 125

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly  
 130 135 140

Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu  
 145 150 155 160

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly  
165 170 175

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr  
180 185 190

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser  
195 200 205

Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp  
210 215 220

Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr  
225 230 235 240

Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp  
245 250 255

Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala  
260 265 270

Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile  
275 280 285

Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val  
290 295 300

Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu  
305 310 315 320

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys  
325 330 335

His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser  
340 345 350

Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe  
355 360 365

Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr  
370 375 380

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe  
385 390 395 400

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys  
405 410 415

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser  
420 425 430

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile  
435 440 445

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly  
450 455 460

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser  
465 470 475 480

Thr Pro Leu Ser His Ser Thr  
485

<210> 27  
<211> 464  
<212> PRT  
<213> Artificial Sequence

*CA* <220>  
<223> Fusion construct of human CD39

<400> 27

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro  
20 25 30

Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr  
35 40 45

Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly  
50 55 60

Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser  
65 70 75 80

Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys  
85 90 95

Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr  
100 105 110

Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu  
115 120 125

Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu  
130 135 140

Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln  
145 150 155 160

Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys  
165 170 175

Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn  
180 185 190

Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln  
195 200 205

Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala  
210 215 220

Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser  
225 230 235 240

Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys  
245 250 255

Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His  
260 265 270

Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro  
275 280 285

Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile  
290 295 300

Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu  
305 310 315 320

Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile  
325 330 335

Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr  
340 345 350

Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu  
355 360 365

Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu  
370 375 380

Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr  
385 390 395 400

Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His  
405 410 415

Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln  
420 425 430

Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn  
435 440 445

Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
450 455 460

<210> 28  
<211> 474  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion construct of human CD39

<400> 28

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu  
20 25 30

Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly  
35 40 45

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys  
50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu  
65 70 75 80

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val  
85 90 95

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu  
100 105 110

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala  
115 120 125

Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp  
130 135 140

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp  
145 150 155 160

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly  
165 170 175

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg  
180 185 190

Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly  
195 200 205

Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln  
210 215 220

Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr  
225 230 235 240

Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys  
245 250 255

Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser  
260 265 270

Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val  
275 280 285

Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu  
290 295 300

Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr  
305 310 315 320

Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys  
325 330 335



Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln  
 340 345 350

Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu  
 355 360 365

Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met  
 370 375 380

Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala  
 385 390 395 400

Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr  
 405 410 415

Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp  
 420 425 430

Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp  
 435 440 445

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln  
 450 455 460

Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470

<210> 29

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion construct of human CD39

<400> 29

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr  
 20 25 30

Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile  
 35 40 45

Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp  
 50 55 60

Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu  
65 70 75 80

Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn  
85 90 95

Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val  
100 105 110

Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr  
115 120 125

Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg  
130 135 140

Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe  
145 150 155 160

Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp  
165 170 175

Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp  
180 185 190

Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala  
195 200 205

Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn  
210 215 220

Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly  
225 230 235 240

Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp  
245 250 255

Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn  
260 265 270

Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val  
275 280 285

Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met  
290 295 300

Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln  
305 310 315 320

Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro  
325 330 335

Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly  
340 345 350

Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn  
355 360 365

Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys  
370 375 380

Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly  
385 390 395 400

Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile  
405 410 415

Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu  
420 425 430

His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr  
435 440 445

Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro  
450 455 460

Leu Ser Thr Pro Leu Ser His Ser Thr  
465 470

<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion construct of human CD39

<400> 30

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15

Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu  
20 25 30

Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser  
35 40 45

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val  
50 55 60

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys  
65 70 75 80

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met  
85 90 95

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro  
100 105 110

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser  
115 120 125

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser  
130 135 140

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu  
145 150 155 160

a2 Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe  
165 170 175

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn  
180 185 190

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val  
195 200 205

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu  
210 215 220

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe  
225 230 235 240

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp  
245 250 255

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro  
260 265 270

Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys  
275 280 285

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln  
290 295 300

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe  
305 310 315 320

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe  
325 330 335

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe  
340 345 350

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys  
355 360 365

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile  
370 375 380

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys  
385 390 395 400

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe  
405 410 415

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly  
420 425 430

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met  
435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
450 455 460

<210> 31

<211> 58

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys  
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly

20

25

30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu  
 35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr  
 50 55

<210> 32  
 <211> 11  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Linker sequence

<400> 32

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser  
 1 5 10

<210> 33  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Linker sequence

<400> 33

Gly Ala Gly Gly Ala Gly Ser Gly Gly Gly Gly Gly Ser  
 1 5 10

<210> 34  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Linker sequence

<400> 34

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 1 5 10

<210> 35  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Linker sequence

<400> 35

Gly Thr Pro Gly Thr Pro Gly Thr Pro  
1 5

<210> 36

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 36

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

*al*

Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser  
20 25

<210> 37

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence

<400> 37

Thr Ser Ser Gly  
1

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